



SEQUENCE LISTING

<110> Honeycutt, Rhonda
McClelland, Michael

<120> A METHOD OF IDENTIFYING TARGET ORGANISMS
BY DETERMINING THE CHARACTERISTICS OF THEIR
INTRONIC REGION NUCLEIC ACIDS

<130> 011399-0005-999

<140> US 10/607,559
<141> 2003-06-25

<150> US 09/645,055
<151> 2000-08-23

<150> US 60/150,977
<151> 1999-08-25

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 <213> *Tilletia horrida*

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<210> 41
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 <213> *Tilletia tritici*

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 gttattcaag acaagtatgg tggttctatc aggcttagat caggtgatcg tacccttcgt 480
 tacagattac aagataaagc tagtgttaatc accttaatac aacatgttaa tggtaacctt 540
 catactcctt taagattaag ccaactacat cgggtatgtc ctctacttaa tatagaggct 600
 aacatgccta taccttaac catatttaat ggttgattta tggcttattt tgatggtaaa 660
 ggttaacatca gatgttagagt acctaataatc tacttaagtg ctacaggtaa agctgcagta 720
 agtcttcaag gttttgtga tgtttttgtt ggtgagatag tataccgttag agccagchat 780
 ggttcatata catggaaact atcccgctga cctagtgtgc tgttattttt gaggtatcag 840
 amatgacata tatcacagtc aacammgcag cggagattgg gcttaatgag aaagtctatc 900
 acttaatttta catggagaaa agtggggatt taaaargatt ttctctgtta aagacatgag 960
 twttatttcca taataaatga aaataaatgc agaagatataa gtccatacgc atcctgaggk 1020
 ttatatcctg attataccag gatttgggat agtwag 1056

<210> 46
 <211> 968
 <212> DNA
 <213> *Candida tropicalis*

<400> 46
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 agagtaaaa ggttaagaga tagtagcaat acttagcgtg atgcagcaga kaaccaacgg 180
 ttcatattcc aagcttattaa tgcctatgaa ctcagtagat atttcagaga ctacacgtgt 240
 aactgtatcc cttcttacgg acccatttcca tcaatgatta gctggcttaa tcgtatgttaa 300
 tggtgccctt aaaatcactc ataaatcaca agttaattgtt gagataatag tgcctcaga 360
 cgagggaaaga atgttaagag ttattcaaga caagtatggt ggttctatca ggcttagatc 420
 aggtgatcgt acccttcgtt acagattaca agataaaagct agtgttaatca ccttaataca 480
 acatgttaat ggttacccctt atactccctt aagattaagc caactacatc gggatgtcc 540
 tctacttaat atagaggctt acatgcctt accttttaccat atatttaatg gttgattttt 600
 gggcttattttt gatgttaag gtaacatcag attagagatc cctaataatctt acttaagtgc 660
 tacaggttaaa gctgcagttaa gtcttcaagg tttttttgtt gttttttgtt gttgagatagt 720
 ataccgttaga gccagchatg gttcatatac atggaaacta tcccgctcgac ctatgtgtgt 780
 gtttattttt aggttatcaga matgacatatac atcacagtca acammgcagc ggagattgg 840
 cttaatgaga aagtctatca ctttaattttac atggagaaaaa gtggggattt aaaargattt 900
 tctctgttaa agacatgagt wttattccat aataaatgaa aataaatgca gaagatataag 960
 tccatacgc 968

<210> 47
<211> 41
<212> DNA
<213> *Candida tropicalis*

<400> 47
gagatcctat tttatatcaa cacctcttct gattcttcgg t

41

<210> 48
<211> 47
<212> DNA
<213> *Candida tropicalis*

<400> 48
catcctgagg kttatatacct gattataccca ggatttggga tagtwag

47

<210> 49
<211> 234
<212> PRT
<213> *Candida tropicalis*

<220>
<221> VARIANT
<222> 4, 193, 214, 222
<223> Xaa = Any Amino Acid

<400> 49
Met Gln Gln Xaa Thr Asn Gly Ser Tyr Ser Lys Thr Leu Met Pro Met
1 5 10 15
Asn Ser Val Asp Ile Ser Glu Thr Thr Arg Val Thr Val Ser Pro Ser
20 25 30
Thr Asp Pro Phe His Gln Trp Leu Ala Gly Thr Ile Asp Ala Asn Gly
35 40 45
Ala Phe Lys Ile Thr His Lys Ser Gln Val Asn Cys Glu Met Met Val
50 55 60
Pro Gln Asn Glu Glu Arg Met Leu Arg Val Ile Gln Asp Lys Tyr Gly
65 70 75 80
Gly Ser Ile Arg Thr Arg Ser Gly Asp Arg Thr Thr Arg Tyr Arg Leu
85 90 95
Gln Asp Lys Ala Ser Val Ile Thr Leu Met Gln His Val Asn Gly Asn
100 105 110
Thr His Thr Pro Leu Arg Leu Ser Gln Thr His Arg Val Cys Pro Thr
115 120 125
Thr Asn Met Glu Ala Asn Met Pro Met Pro Leu Thr Met Phe Asn Gly
130 135 140
Trp Phe Met Gly Tyr Phe Asp Gly Lys Gly Asn Ile Arg Cys Arg Val
145 150 155 160
Pro Asn Ile Tyr Leu Ser Ala Thr Gly Lys Ala Ala Val Ser Thr Gln
165 170 175
Gly Phe Val Asp Val Phe Gly Gly Glu Met Val Tyr Arg Arg Ala Ser
180 185 190
Xaa Gly Ser Tyr Thr Trp Lys Thr Ser Arg Arg Pro Ser Val Thr Leu
195 200 205
Phe Met Arg Tyr Gln Xaa Trp His Met Ser Gln Ser Thr Xaa Gln Arg
210 215 220
Arg Leu Gly Leu Met Arg Lys Ser Ile Thr
225 230

<210> 50
<211> 156

<212> PRT

<213> Tilletia horrida

<400> 50

Met Asn Tyr Thr Val Cys Trp Lys Tyr Thr Phe Asn Val Ile Ser Thr
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Ile Ile Met Arg Gly Ile Ile Thr Ser Met Ser Arg Tyr Ser Lys Asn
20 25 30
Glu Met Thr Lys Met Gln Ser Ala Gly Asn Gln Arg Arg Ser Met Ser
35 40 45
Ser Thr Val Gly Thr Thr Glu Thr Met Arg Val Thr Thr Phe Ser Thr
50 55 60
Thr Phe Gly Gln Trp Thr Ala Gly Val Ile Asp Gly Asp Gly Ser Thr
65 70 75 80
Gln Thr Ser Lys Gln Gly Tyr Thr Ser Thr Glu Ile Thr Met Gly Thr
85 90 95
Glu Asp Thr Pro Thr Thr Arg Tyr Ile Gln Asp Lys Thr Gly Gly Ser
100 105 110
Ile Lys Met Arg Thr Glu Ala Lys Ala Tyr Arg Tyr Arg Thr His Asn
115 120 125
Lys Arg Gly Met Ile Thr Met Ile Asn Tyr Met Asn Gly Asn Ile Arg
130 135 140
His Ser Ser Arg Thr Thr Gln Thr His Arg Val Cys
145 150 155

<210> 51

<211> 115

<212> PRT

<213> Tilletia horrida

<400> 51

Met Glu Pro Ile Pro Thr Thr Asn Asp Asn Tyr Trp Phe Ala Gly Phe
1 5 10 15
Phe Asp Ala Glu Gly Thr Ile Thr Phe Ser Phe Lys Asn Glu Tyr Pro
20 25 30
Gln Thr Ser Met Arg Val Ser Asn Lys Asn Met Glu Asp Val Gln Trp
35 40 45
Tyr Lys Asn Met Phe Gly Gly Tyr Ile Tyr Phe Asp Ser Ser Gln Tyr
50 55 60
Gly His Tyr Gln Trp Ser Val Gln Arg Arg Asn Asp Val Met Arg Met
65 70 75 80
Arg Arg Tyr Phe Lys Asn Lys Cys Lys Ser His Lys Ser Asn Arg Phe
85 90 95
Phe Thr Met Ser Asp Tyr Tyr Gln Thr Ser Asp Thr Lys Ala Tyr Lys
100 105 110
Lys Glu Ser
115

<210> 52

<211> 1547

<212> DNA

<213> Lycoperdon pyriforme

<220>

<221> misc_feature

<222> 362

<223> n = A,T,C or G

<400> 52

ctcttaggata aaatatagtt gtgaataaga attgttttg taacatgtga taaggagatc 60
atcgattctt aagctgttcg agggcgctcg gaaaggtaa accgtgtaaa aactgtgaaa 120

tgcattgc aaaaggattg cgattccgag gatcagttag gaaaaatcta accgatcacc 180
 ctaaaagcct tcctctgcca tcgaaatatt agtgtcagc accttgcga taaaagcact 240
 aatgtttc atgtgaacta gatgtcaag aattcatata agttgcttga gatccaaac 300
 cagcacatta atttgcctt gttgcttgc cagcaaaaca tcaacttctg ttgcggcac 360
 anacgtgacg atcaacgaga taaattacct ttagattaaa agtgttgcatt tgtagatcg 420
 aaacgaaata aagaacttcg gaaattgtt tctagtaaca gaaaccatg agttcgcat 480
 cttgaatttg gcagtgacta atgaggatga tctgattcgt atgtgcataa aaccaatcgt 540
 ccaaaatgtc tgcgacttcc aacgaagtt acgagtaata atccatttag tttgcgcata 600
 tctaaggcta aagaagatcg tgttttcctt ctcaatttag attgacatga ctgtgtcgaa 660
 tgatttgcatt aacccacaca acaagcatta gtgagatttgc accctcatat gcttaattga 720
 cagttaccac gagcttgca ccttgctcat aagttataa agctatgagt aggcaatgtt 780
 tggtttttc gattaagcat ggttataacc gcttcaag tacgaagata ggaatttcct 840
 cttgtagaca atggctcag agctcgctgt gacttgcgt ttcgtcgatg ataattattg 900
 tacttaatca catgttgggt tgcccttatt tccttcacca agttacattaa tagagaatgg 960
 atggtccgat tgatctaattc tctgttcaac actttgagat tatccgtcca cagataaaat 1020
 taagatttctt ggacaatctc acttattata aatatggta taagatcagg tataatatgt 1080
 ccaacacatt agaaaatctctt tttgtcgaa tcgaaacaa cgtcgctcgt tcgattattt 1140
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 cagttgcaaa cgagcttggc tctggcagcc atcaaatttg atagcgatgt ctgaccgcgt 1260
 gaacacccac ggactttcc acgaattaca tgtcagctaa ggaatataat gtgttccgat 1320
 aacacgagaa atactctaattt ccaaaaatcc aagttgtcg gtttcggctcg tcatcaaattc 1380
 cgtgaaagcg ctcggattta gatggacccg atgacccgat aattcgtagg tcggatgtta 1440
 tcatgtaccc gggatctctc tcgattattt agatccaaa atcccctacc caaaaaaaaacca 1500
 gtaggtcttc aaatataaaa ttaatatggt cctaaaccct atcatac 1547

<210> 53
 <211> 203
 <212> PRT
 <213> Lycoperdon pyriforme

<220>
 <221> VARIANT
 <222> 181
 <223> Xaa = Any Amino Acid

<400> 53
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 Gly Asn Arg Cys Ser Pro Leu Arg Met Glu Ala Trp Thr Ser Arg His
 20 25 30
 Ile Trp Tyr Glu Leu Ala Phe Leu Val Cys Asn Gly Trp Val Ser Lys
 35 40 45
 Tyr Leu Asn Thr Arg Ser Thr Phe Arg Ala Pro Leu Thr Val Asn Ser
 50 55 60
 Tyr Thr Pro Ser Leu Glu Trp Leu Arg Thr Pro Pro Met Ser Leu
 65 70 75 80
 Val Ser Cys Val Ser Thr Val Arg Leu Thr Ser Pro Phe Cys Ala Arg
 85 90 95
 Arg Asn Arg Asn Thr Tyr Ala Phe Glu Leu Pro Asn Asn Glu Gln Leu
 100 105 110
 Lys Gln Pro Ser Ala Ser Val Lys Pro Ala Asn Gln Lys Ser Cys Met
 115 120 125
 Thr Ser Thr Val Gly Val Ile Ser Asp Gly Leu Ser Ser Thr Ala Trp
 130 135 140
 Val Ala Lys Asp Asn Asp Thr Leu Leu Lys Ala Ser Arg Asn Lys Ala
 145 150 155 160
 Lys Thr Asp Cys Leu Val Val Lys Ile Arg Phe Pro Leu Asn Arg Ala
 165 170 175
 Thr Ser Ser Ala Xaa Thr Gly Val Val Phe Asn Tyr Lys Thr Thr Ser
 180 185 190
 Ser Leu Ser Leu Phe Asn Tyr Thr Lys Thr
 195 200

<210> 5
<211> 225
<212> PRT
<213> Tilletia indica

<400> 54
Met Ser Thr Arg Gly Asn Cys Met Phe Val Ile Thr Gln Ser Thr Lys
1 5 10 15
Asp Ile Gln Val Thr His Phe Ile Gln Asp Lys Thr Gly Phe Gly Arg
20 25 30
Val Ile Lys Gln Gly His Ser Thr Ser Arg Phe Ile Val Gln Asp Asn
35 40 45
Lys Asn Thr Tyr Thr Thr His Thr Phe Asn Gly Asn Thr Val Thr
50 55 60
Pro Thr Lys Met Glu Ser Phe Lys Lys Phe Met Glu Met Phe Ile Lys
65 70 75 80
Asn Ser Ser Asn Tyr Ser Ile Thr Pro Ile Ser Val Trp Arg Thr Thr
85 90 95
Pro Ser Cys Asn Asp Ala Trp Ile Ser Gly Phe Thr Asp Ala Glu Gly
100 105 110
Cys Phe Thr Cys Ser Thr Thr Gly Asn Ser Thr Ala Tyr Arg Phe Arg
115 120 125
Phe Met Thr Ser Gln Lys Asn Glu Lys Asn Lys Cys Val Thr Asp His
130 135 140
Ile Ala Phe Thr Thr Asn Gly Lys Val Arg Pro His Ser Ile Gln Gly
145 150 155 160
Val Tyr Glu Thr Thr Val Asn Gly Ile Cys Asn Asn Lys Gly Val Val
165 170 175
Gln Tyr Phe Asp Lys Tyr Lys Thr Tyr Thr Lys Lys Ala Ser Ser Tyr
180 185 190
Thr Thr Trp Lys Glu Val Ser Glu Asp Thr Lys Asp Gly Lys His Thr
195 200 205
Ser Glu Ser Thr Arg Thr Ile Met Lys Glu Lys Val Met Lys Ile Asn
210 215 220
Ser
225

<210> 55
<211> 1481
<212> DNA
<213> Aspergillus niger

<400> 55
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taacaattct agcttcaata gtaaagatta ataaatcaaa tttaaatgtttt aaatttaatt 120
atagtacttt cataaataaa tttrattttt caaattttta tataaaatttt tctaattttt 180
tacctaataaa tactttacct tcagaaaaat tcttgacttg attttatagga ttccacagaag 240
gtgagggggtc atttatagta aataatagag gtatctttt ttttggattt acacaaaaaaa 300
ctatagatat taaaatattttaa gaatttataa aagaaactttt aggtttgggt aaagtaattc 360
aacaatctaa attaactagt agatatgtt cacaacaaa aaaagaaata gaaataacttta 420
ttcattttgtt taatggtaat ctttatattac caagtagaaaa gataaaatttt gaaaatttca 480
ttaaaggatt taatatttga ataggtaaag gttagataaaa attagatctt gttgaatttt 540
aacataattt tattttacct agtttaataa atagttgatt ggcagggtttt actgtatgggg 600
aaggctgtt tacttggct ataggtaaag acaaaggatt tagtttaat ttaatattt 660
ctcaaaaatg agaggaaaat attgaagtat tacaacatct ttgtactttt ttaatggag 720
gaatagtctc aaaacatagt gtggataatg taaatgaatt tagaatagga ggattaaaaaa 780
attgtaaaaaa tatatttccc tattttgata cttatacattt attaactaaa aaatctacta 840
gttataatttt atgaaaagaa atatatgaag attgttaaa aaaatatcat tttagacccaa 900
ttaaagggtt agagatgatt gaaaaagcta gattgataaa taaaattaat taattttttt 960
attagggaaa aaaagtaaag gtttaacgtt caagttttga agctctttagg acagatgtaa 1020
aaggatataa gatccaaaag agcaaatattt ctataatgaa tataccttat acttagttaa 1080
tgtttagtta ttactacttg caactcttaa gtgttaacgttataataattt ggtatataattt 1140

gttataactta	tcaattaata	tataattgat	aaaaggaaaa	gttagtataa	acattagcga	1200
tactagtgtt	aacggtaat	aaattttcat	gtttaaagac	cgtcggttat	ttaagtgacc	1260
gctacagact	ggttcaactgg	taggtggctg	aatgctgt	taatgtacag	tcggttcctt	1320
ccatatttta	tatatgcaca	agcccagaat	tatataatta	ctggtacctg	gatttaataa	1380
atgaacatca	atataattgat	gagaagttaa	atttgaagga	atggattctt	cggacatccg	1440
gaagtttaca	tcttaattat	accaggattt	gggatagtaa	g		1481

<210> 56
<211> 1393
<212> DNA
<213> Aspe

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<210> 57
<211> 30
<212> DNA
<213> Aspergillus niger
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<400> 57
qagatcctat tttatatcaa catctttct

30

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<210> 58
<211> 58
<212> DNA
<213> Aspergillus niger
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<400> 58
qattcttcgg acatcccqaa qtttacatct taattatacc aggatttggg ataqtaaq 58

<210> 59
<211> 316
<212> PRT
<213> *Aspergillus flavus*

<220>
<221> VARIANT

<222> 48, 203

<223> Xaa = Any Amino Acid

<400> 59

Asp	Pro	Ile	Leu	Tyr	Gln	His	Leu	Phe	Ser	Arg	Asp	Ile	Leu	Ile	Asn
1				5				10						15	
Cys	Leu	Ile	Leu	Thr	Ile	Leu	Ala	Ser	Ile	Val	Lys	Ile	Asn	Lys	Ser
				20				25					30		
Asn	Leu	Ser	Phe	Lys	Phe	Asn	Tyr	Ser	Thr	Phe	Ile	Asn	Lys	Phe	Xaa
				35			40					45			
Phe	Ser	Asn	Phe	Tyr	Ile	Lys	Phe	Ser	Asn	Tyr	Leu	Pro	Asn	Asn	Thr
				50		55				60					
Leu	Pro	Ser	Glu	Lys	Phe	Leu	Thr	Trp	Phe	Ile	Gly	Phe	Thr	Glu	Gly
				65		70			75				80		
Glu	Gly	Ser	Phe	Ile	Val	Asn	Asn	Arg	Gly	Asp	Leu	Cys	Phe	Val	Ile
					85			90					95		
Thr	Gln	Lys	Thr	Ile	Asp	Ile	Glu	Ile	Leu	Glu	Phe	Ile	Lys	Glu	Thr
				100			105						110		
Leu	Gly	Phe	Gly	Lys	Val	Ile	Gln	Gln	Ser	Lys	Leu	Thr	Ser	Arg	Tyr
				115			120				125				
Val	Thr	Gln	Asn	Lys	Lys	Glu	Ile	Glu	Ile	Leu	Ile	His	Leu	Phe	Asn
				130		135			140						
Gly	Asn	Leu	Ile	Leu	Pro	Ser	Arg	Lys	Ile	Lys	Phe	Glu	Asn	Phe	Ile
				145		150			155				160		
Lys	Gly	Phe	Asn	Ile	Trp	Ile	Gly	Lys	Gly	Arg	Ile	Lys	Leu	Asp	Pro
					165			170				175			
Val	Glu	Leu	Lys	His	Asn	Phe	Ile	Leu	Pro	Ser	Leu	Asn	Asn	Ser	Trp
				180			185					190			
Leu	Ala	Gly	Phe	Thr	Asp	Gly	Glu	Gly	Cys	Xaa	Thr	Cys	Ser	Ile	Gly
				195			200				205				
Lys	Asp	Lys	Gly	Phe	Ser	Phe	Asn	Phe	Asn	Ile	Ala	Gln	Lys	Trp	Glu
				210		215				220					
Glu	Asn	Ile	Glu	Val	Leu	Gln	His	Leu	Cys	Thr	Leu	Phe	Asn	Gly	Gly
				225		230			235				240		
Ile	Val	Ser	Lys	His	Ser	Val	Asp	Asn	Val	Asn	Glu	Phe	Arg	Ile	Gly
					245			250				255			
Gly	Leu	Lys	Asn	Cys	Lys	Asn	Ile	Phe	Pro	Tyr	Phe	Asp	Thr	Tyr	Thr
					260			265				270			
Leu	Leu	Thr	Lys	Lys	Ser	Thr	Ser	Tyr	Ile	Leu	Trp	Lys	Glu	Ile	Tyr
				275			280				285				
Glu	Asp	Leu	Leu	Lys	Lys	Tyr	His	Leu	Asp	Pro	Ile	Lys	Arg	Val	Glu
				290		295			300						
Met	Ile	Glu	Lys	Ala	Arg	Leu	Ile	Asn	Lys	Ile	Asn				
				305		310			315						